

0590
0821

AL O/PE

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 10/9/2001
Edited by: AL
Verified by: AL (STIC staff)

Serial Number: 09/925139

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

2/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/925,139

DATE: 10/09/2001
TIME: 18:03:30

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\10092001\I925139.raw

```

3 <110> APPLICANT: Rosanne M. Crooke
4      Mark J. Graham
5      Pam Nero
6      Edward Wancewicz
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN
EXPRESSION
11 <130> FILE REFERENCE: ISPH-0596
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/925,139
C--> 13 <141> CURRENT FILING DATE: 2001-08-08
13 <160> NUMBER OF SEQ ID NOS: 50
15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 20
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctcttcaggg                20
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 20
30 <212> TYPE: DNA
31 <213> ORGANISM: Artificial Sequence
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Antisense Oligonucleotide
36 <400> SEQUENCE: 2
37 atgcattctg cccccaagga                20
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 1787
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens.
44 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION: (131)...(1612)
48 <400> SEQUENCE: 3
49 gtgaatctct ggggccagga agaccctgct gcccggaaga gcctcatgtt ccgtgggggc 60
50 tgggaggaca tacatatacg ggctccaggc tgaacggctc gggccactta cacaccactg 120
51 cctgataacc atg ctg gct gcc aca gtc ctg acc ctg gcc ctg ctg ggc 169
52      Met Leu Ala Ala Thr Val Leu Thr Leu Ala Leu Leu Gly
53      1              5              10
55 aat gcc cat gcc tgc tcc aaa ggc acc tcg cac gag gca ggc atc gtg 217
56 Asn Ala His Ala Cys Ser Lys Gly Thr Ser His Glu Ala Gly Ile Val
57      15              20              25
59 tgc cgc atc acc aag cct gcc ctg ctg gtg ttg aac cac gag act gcc 265
60 Cys Arg Ile Thr Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala
61      30              35              40              45
63 aag gtg atc cag acc gcc ttc cag cga gcc agc tac cca gat atc acg 313
64 Lys Val Ile Gln Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr

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65 314          50          55          60
67 ggc gag aag gcc atg latg ctc ctt ggc caa gtc aag tat ggg ttg cac 361
68 Gly Glu Lys Ala Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His
69          65          70          75
71 aac atc cag atc agc cac ttg tcc atc gcc agc agc cag gtg gag ctg 409
72 Asn Ile Gln Ile Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu
73          80          85          90
75 gtg gaa gcc aag tcc att gat gtc tcc att cag aac gtg tct gtg gtc 457
76 Val Glu Ala Lys Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val
77          95          100          105
79 ttc aag ggg acc ctg aag tat ggc tac acc act gcc tgg tgg ctg ggt 505
80 Phe Lys Gly Thr Leu Lys Tyr Gly Tyr Thr Ala Trp Trp Leu Gly
81 110          115          120          125
83 att gat cag tcc att gac ttc gag atc gac tct gcc att gac ctc cag 553
84 Ile Asp Gln Ser Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln
85          130          135          140
87 atc aac aca cag ctg acc tgt gac tct ggt aga gtg cgg acc gat gcc 601
88 Ile Asn Thr Gln Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala
89          145          150          155
91 cct gac tgc tac ctg tct ttc cat aag ctg ctc ctg cat ctc caa ggg 649
92 Pro Asp Cys Tyr Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly
93          160          165          170
95 gag cga gag cct ggg tgg atc aag cag ctg ttc aca aat ttc atc tcc 697
96 Glu Arg Glu Pro Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser
97          175          180          185
99 ttc acc ctg aag ctg gtc ctg aag gga cag atc tgc aaa gag atc aac 745
100 Phe Thr Leu Lys Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn
101 190          195          200          205
103 gtc atc tct aac atc atg gcc gat ttt gtc cag aca agg gct gcc agc 793
104 Val Ile Ser Asn Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser
105          210          215          220
107 atc ctt tca gat gga gac att ggg gtg gac att tcc ctg aca ggt gat 841
108 Ile Leu Ser Asp Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp
109          225          230          235
111 ccc gtc atc aca gcc tcc tac ctg gag tcc cat cac aag ggt cat ttc 889
112 Pro Val Ile Thr Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe
113          240          245          250
115 atc tac aag aat gtc tca gag gac ctc ccc ctc ccc acc ttc tcg ccc 937
116 Ile Tyr Lys Asn Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro
117          255          260          265
119 aca ctg ctg ggg gac tcc cgc atg ctg tac ttc tgg ttc tct gag cga 985
120 Thr Leu Leu Gly Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg
121 270          275          280          285
123 gtc ttc cac tcg ctg gcc aag gta gct ttc cag gat ggc cgc ctc atg 1033
124 Val Phe His Ser Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met
125          290          295          300
127 ctc agc ctg atg gga gac gag ttc aag gca gtg ctg gag acc tgg ggc 1081
128 Leu Ser Leu Met Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly
129          305          310          315

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131 ttc aac acc aac cag gaa atc ttc caa gag gtt gtc ggc ggc ttc ccc 1129
132 Phe Asn Thr Asn Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro
133      320      325      330
135 agc cag gcc caa gtc acc gtc cac tgc ctc aag atg ccc aag atc tcc 1177
136 Ser Gln Ala Gln Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser
137      335      340      345
139 tgc caa aac aag gga gtc gtg gtc aat tct tca gtg atg gtg aaa ttc 1225
140 Cys Gln Asn Lys Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe
141 350      355      360      365
143 ctc ttt cca cgc cca gac cag caa cat tct gta gct tac aca ttt gaa 1273
144 Leu Phe Pro Arg Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu
145      370      375      380
147 gag gat atc gtg act acc gtc cag gcc tcc tat tct aag aaa aag ctc 1321
148 Glu Asp Ile Val Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu
149      385      390      395
151 ttc tta agc ctc ttg gat ttc cag att aca cca aag act gtt tcc aac 1369
152 Phe Leu Ser Leu Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn
153      400      405      410
155 ttg act gag agc agc tcc gag tcc atc cag agc ttc ctg cag tca atg 1417
156 Leu Thr Glu Ser Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met
157      415      420      425
159 atc acc gct gtg ggc atc cct gag gtc atg tct cgg ctc gag gta gtg 1465
160 Ile Thr Ala Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val
161 430      435      440      445
163 ttt aca gcc ctc atg aac agc aaa ggc gtg agc ctc ttc gac atc atc 1513
164 Phe Thr Ala Leu Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile
165      450      455      460
167 aac cct gag att atc act cga gat ggc ttc ctg ctg ctg cag atg gac 1561
168 Asn Pro Glu Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp
169      465      470      475
171 ttt ggc ttc cct gag cac ctg ctg gtg gat ttc ctc cag agc ttg agc 1609
172 Phe Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
173      480      485      490
175 tag aagtctccaa ggaggtcggg atggggcttg tagcagaagg caagcaccag 1662
177 gctcacagct ggaacctgg tgtctctcc agcgtggtg aagttgggtt aggagtacgg 1722
178 agatggagat tggctcccaa ctctcccta tctaaaggc ccactggcat taaagtgtg 1782
179 tatcc 1787
181 <210> SEQ ID NO: 4
182 <211> LENGTH: 20
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: PCR Primer
189 <400> SEQUENCE: 4
190 tcgacatcat caaccctgag 20
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 20
194 <212> TYPE: DNA
195 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/925,139

DATE: 10/09/2001
 TIME: 18:03:30

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF3\10092001\I925139.raw

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197 <220> FEATURE:
198 <223> OTHER INFORMATION: PCR Primer
200 <400> SEQUENCE: 5
201 ctaacccaac ttccaccacg 20
203 <210> SEQ ID NO: 6
204 <211> LENGTH: 49
205 <212> TYPE: DNA
206 <213> ORGANISM: Artificial Sequence
208 <220> FEATURE:
209 <223> OTHER INFORMATION: PCR Probe
211 <400> SEQUENCE: 6
212 cctgagcacc tgctggtgga tttcctccag agcttgagct agaagtctc 49
214 <210> SEQ ID NO: 7
215 <211> LENGTH: 19
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: PCR Primer
222 <400> SEQUENCE: 7
223 gaaggtgaag gtcggagtc 19
225 <210> SEQ ID NO: 8
226 <211> LENGTH: 20
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: PCR Primer
233 <400> SEQUENCE: 8
234 gaagatggtg atgggatttc 20
236 <210> SEQ ID NO: 9
237 <211> LENGTH: 20
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial Sequence
241 <220> FEATURE:
242 <223> OTHER INFORMATION: PCR Probe
244 <400> SEQUENCE: 9
245 caagcttccc gttctcagcc 20
247 <210> SEQ ID NO: 10
248 <211> LENGTH: 20
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Antisense Oligonucleotide
255 <400> SEQUENCE: 10
256 aacatgaggc tcttcgggc 20
258 <210> SEQ ID NO: 11
259 <211> LENGTH: 20
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:

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DATE: 10/09/2001

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Input Set : A:\PTO.AMC.txt

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264 <223> OTHER INFORMATION: Antisense Oligonucleotide
266 <400> SEQUENCE: 11
267 gcctggagcc cgtatatgta 20
269 <210> SEQ ID NO: 12
270 <211> LENGTH: 20
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Antisense Oligonucleotide
277 <400> SEQUENCE: 12
278 taagtggccc gagccgttca 20
280 <210> SEQ ID NO: 13
281 <211> LENGTH: 20
282 <212> TYPE: DNA
283 <213> ORGANISM: Artificial Sequence
285 <220> FEATURE:
286 <223> OTHER INFORMATION: Antisense Oligonucleotide
288 <400> SEQUENCE: 13
289 cagccagcat ggttatcagg 20
291 <210> SEQ ID NO: 14
292 <211> LENGTH: 20
293 <212> TYPE: DNA
294 <213> ORGANISM: Artificial Sequence
296 <220> FEATURE:
297 <223> OTHER INFORMATION: Antisense Oligonucleotide
299 <400> SEQUENCE: 14
300 gcatgggcat tgcccagcag 20
302 <210> SEQ ID NO: 15
303 <211> LENGTH: 20
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Antisense Oligonucleotide
310 <400> SEQUENCE: 15
311 gcacacgatg cctgcctcgt 20
313 <210> SEQ ID NO: 16
314 <211> LENGTH: 20
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Antisense Oligonucleotide
321 <400> SEQUENCE: 16
322 atcatggcct tctgcccgt 20
324 <210> SEQ ID NO: 17
325 <211> LENGTH: 20
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: Antisense Oligonucleotide

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VERIFICATION SUMMARY

PATENT APPLICATION: . US/09/925,139

DATE: 10/09/2001

TIME: 18:03:31

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10092001\I925139.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date